The intestinal stem cell markers Bmi1 and Lgr5 identify two functionally distinct populations

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The small intestine epithelium undergoes rapid and continuous regeneration supported by crypt intestinal stem cells (ISCs). Bmi1 and Lgr5 have been independently identified to mark long-lived multipotent ISCs by lineage tracing in mice; however, the functional distinctions between these two populations remain undefined. Here, we demonstrate that Bmi1 and Lgr5 mark two functionally distinct ISCs in vivo. Lgr5 marks mitotically active ISCs that exhibit exquisite sensitivity to canonical Wnt modulation, contribute robustly to homeostatic regeneration, and are quantitatively ablated by irradiation. In contrast, Bmi1 marks quiescent ISCs that are insensitive to Wnt perturbations, contribute weakly to homeostatic regeneration, and are resistant to high-dose radiation injury. After irradiation, however, the normally quiescent Bmi1+ ISCs dramatically proliferate to clonally repopulate multiple contiguous crypts and villi. Clonogenic culture of isolated single Bmi1+ ISCs yields long-lived self-renewing spheroids of multiple contiguous crypts and villi. Clonogenic culture of isolated single Bmi1+ ISCs yields long-lived self-renewing spheroids of intestinal epithelium that produce Lgr5-expressing cells, thereby establishing a lineage relationship between these two populations in vitro. Taken together, these data provide direct evidence that Bmi1 marks quiescent, injury-inducible reserve ISCs that exhibit striking functional distinctions from Lgr5+ ISCs and support a model whereby distinct ISC populations facilitate homeostatic vs. injury-induced regeneration.

R-spondin | Dickkopf-1 | intestinal regeneration

The G protein-coupled receptor Lgr5 and the Polycomb group protein Bmi1 are two recently described molecular markers of self-renewing and multipotent adult stem cell populations residing in the crypt of the small intestine, capable of supporting regeneration of the intestinal epithelium (1, 2). Despite their similar ability to functionally repopulate the intestinal epithelium as demonstrated by independent in vivo lineage tracing experiments in reporter mice, the intestinal stem cells (ISCs) identified by these two molecular markers are spatially distinct. Whereas Lgr5+ ISCs are crypt base columnar (CBC) cells (1, 3) interspersed between Paneth cells and expressed throughout the intestine, Bmi1+ ISCs are mostly restricted to the +4 cell position abutting the uppermost Paneth cell in proximal small intestine crypts (2). Lgr5+ ISCs are actively cycling (1), equipotent, and contribute to intestinal homeostasis by neutral drift competition (4–6). By comparison, Bmi1+ ISCs are less well characterized, and because of the lack of direct evidence, their cell cycle status is variably ascribed to be rapidly (7) vs. slowly cycling (8). It has been suggested that Bmi1 and Lgr5 mark an overlapping and possibly identical or redundant population of ISCs (5, 7, 9); however, no direct exploration of their functional similarities and differences has been performed. Further, it is unknown how Bmi1+ and Lgr5+ ISCs relate to a proposed model in which the intestine differentially uses an actively cycling ISC population during homeostasis and a distinct quiescent, injury-induced ISC population (10, 11) during epithelial repair. We therefore conducted a systematic comparison of Bmi1+ and Lgr5+ ISC function during homeostasis and injury repair to investigate whether Lgr5 and Bmi1 mark identical, similar, or distinct ISC populations.

Results

Bmi1 Marks Quiescent ISCs That Contribute Minimally to Intestinal Homeostasis. Given the spatial localization of Bmi1+ ISCs at the +4 position, where a DNA label-retaining cell has also been described (12, 13), we postulated that Bmi1 marks a quiescent ISC. Lgr5-eGFP-RES-CreERT2 and Bmi1-CreER; Rosa26-YFP mice were used to compare the basal proliferation status of Lgr5+ vs. Bmi1+ ISCs during homeostasis. We used short-term tamoxifen exposure, for induction of Cre-mediated recombination, to selectively mark Bmi1+ ISCs in vivo. Accordingly, Bmi1-CreER; Rosa26-YFP mice were treated with tamoxifen 1–2 d before killing to genetically label Bmi1+ cells with YFP, revealing one to two YFP+ cells at approximately the +4 cell position (ranging from +1 to +6) within ±10% of proximal small intestine crypts, in agreement with previous reports (2). To determine basal proliferation status, labeling of actively cycling S phase cells was performed by using the thymidine analog 5-ethyl-2’-deoxyuridine (EdU). Under steady-state conditions, histological examination of small intestine revealed 31 ± 5.2% EdU incorporation among Lgr5+ ISCs, identified as GFP+ CBC cells in Lgr5-eGFP-RES-CreERT2 mice. In contrast, only 1.7 ± 0.30% of Bmi1+ ISCs, identified by the crypt Rosa-YFP signal after 1.5-d tamoxifen exposure in Bmi1-CreER; Rosa26-YFP mice, incorporated EdU (Fig. 1 A–F and N). To examine the relative contribution of Lgr5 vs. Bmi1 ISCs to tissue regeneration under steady-state conditions, lineage tracing was induced by tamoxifen administration in Cre reporter mice to mark the ISCs and their respective progeny. Upon tamoxifen-mediated lineage tracing of Lgr5+ and Bmi1+ ISCs in Lgr5-eGFP-RES-CreERT2; Rosa26-TdTomato and Bmi1-CreER; Rosa26-YFP mice, Lgr5+ ISCs were markedly more efficient at generating progeny than Bmi1+ ISCs by 7 d of lineage tracing with 95 ± 1.7% vs. 18 ± 5.1% lineage “stripe” generation, respectively (Fig. 1 G–I). This method also likely underestimates their substantial relative difference in progeny generation because of the more qualitatively vigorous nature of Lgr5 stripping. Overall, these differences in basal proliferation and lineage-forming efficiency reflect a much greater functional contribution of Lgr5+ ISCs to homeostatic small intestine regeneration compared with Bmi1+ ISCs.


The authors declare no conflict of interest.

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Differential Responses of Bmi1+ vs. Lgr5+ ISCs to Canonical Wnt Modulation. Because Lgr5+ and Bmi1+ ISCs reside in spatially distinct crypt locations, we explored whether they exhibited differential responses to global modulation of the canonical Wnt pathway, which is required to maintain adult intestine epithelial proliferation and crypt architecture (14–16). Gain- and loss-of-function manipulation of the canonical Wnt signaling pathway was achieved in mice by using adenoviral expression of the soluble, secreted factors R-Spondin1 (Rspo1) (17, 18) and Dickkopf-1 (Dkk1) (14), respectively. A single i.v. injection of adenovirus encoding either the Wnt agonist Rspo1 or antagonist Dkk1 results in hepatic infection and transduction, secretion of the recombinant factor into the systemic circulation, and leads to profound histological changes in the intestinal epithelium within 5 d after infection (14). In Lgr5-eGFP-IRESCreERT2 and Bmi1-CreER; Rosa26-YFP mice, canonical Wnt signaling was potently induced by systemic administration of an adenovirus encoding Rspo1 fused to an IgG2α Fc fragment (Ad Rspo1-Fc), causing marked crypt hypertrophy and hyperproliferation. By 5 d after infection, Ad Rspo1-Fc markedly expanded Lgr5-eGFP+ cells, and expression of the surrogate marker Olfm4 (7), which was not seen with a control adenovirus encoding IgG2α Fc (Ad Fc) (Fig. 1 J, K, U, and V and Fig. S1 A and B). Electron microscopy of Ad Rspo1-Fc–treated small intestine confirmed expansion of multiple consecutive slender CBC cells between Paneth cells, consistent with substantially increased numbers of
Lgr5+ ISCs, compared with only single CBC cells between Paneth cells with Ad Fc treatment (Fig. 1 O and P). In contrast, Ad Rspo1-Fc treatment did not significantly alter either the relative abundance or the mitotic index of Bmi1+ ISCs labeled with 1- or 2-d tamoxifen exposure in Bmi1-CreER; Rosa26-YFP mice (Fig. 1 L–N and Fig. S1 D and E). Further, Ad Rspo1-Fc did not enhance the basal level of infrequent lineage stripes arising from Bmi1+ ISCs despite dramatic concurrent expansion of the crypt compartment (Fig. S1 G–I) and Lgr5-eGFP+ cells (Fig. 1K).

Consistently, systemic Wnt loss-of-function studies were performed in these reporter mice by using adenosivirus encoding Dkk1 (Ad Dkk1), which has been reported to induce rapid crypt loss and destruction of the small intestine epithelial architecture (14) (Fig. 1 Q–T). Correspondingly, Ad Dkk1 induced a profound loss of Lgr5-eGFP and Olfm4 expression in the small intestine crypts (Fig. 1 Q, R, U, and W and Fig. S1 A and C). In contrast to the dramatic effect on Lgr5+ ISCs, Ad Dkk1 treatment did not significantly diminish 1- or 2-d tamoxifen-labeled Bmi1+ ISCs in Bmi1-CreER; Rosa26-YFP mice, which, in fact, persisted despite Ad Dkk1-mediated crypt loss (Fig. 1 S and T and Fig. S1 D and F). Thus, the Lgr5-eGFP+ but not the Bmi1+ ISC population exhibited exquisite sensitivity to global gain- and loss-of-function Wnt signaling modulation mediated by Rspos1 and Dkk1, respectively, highlighting substantial functional differences between the response of these two ISC populations to extracellular Wnt signals.

**Differential Responses of Bmi1+ vs. Lgr5+ ISCs to Radiation Injury.** We further probed the functional differences between Lgr5+ and Bmi1+ ISCs by using a radiation injury model. Lgr5-eGFP-IRES-CreERT2 and Bmi1-CreER; Rosa26-YFP mice were treated with 12 Gy whole-body irradiation. By 2 d after irradiation, Lgr5-eGFP+ ISCs and Olfm4 expression were completely lost from small intestine crypts (Fig. 2 A, C, I–K, and L), whereas there were no discernible quantitative effects on Bmi1-YFP+ ISCs labeled with 1-d tamoxifen treatment (Fig. 2 B and D). By 4.5 and 7 d after irradiation, rare Lgr5-eGFP+ cells reemerged, scattered sporadically throughout the small intestine at a frequency of ≈1/180 total crypts, but these were still severely diminished compared with unirradiated littermate controls (Fig. 2 E and G). In contrast, irradiation induced a strong proliferative response in 1-d tamoxifen-treated Bmi1+ ISCs, 17 ± 1.5% of which were robustly labeled with EdU by 2 d after irradiation, compared with 1.7 ± 0.30% during homeostasis (Fig. 2 O–R); this increased proliferation was accompanied by a fivefold expansion in Bmi1+ YFP+ ISCs/progeny upon fluorescence-activated cell sorting (FACS) analysis by 4.5 d after irradiation vs. unirradiated littermate controls (Fig. 2 M and N).

We also examined the functional effects of irradiation on the ability of Lgr5+ vs. Bmi1+ ISCs to generate downstream progeny. Two serial tamoxifen injections in Lgr5-eGFP-IRES-CreERT2; Rosa26-YFP mice, 1 d before and 1 d after irradiation, were used to irreversibly mark the Lgr5+ lineage with YFP, in a manner independent of concurrent Lgr5 expression. Accordingly, both YFP-marked Lgr5+ cells and their downstream progeny were eradicated by 4.5 and 7 d after irradiation (Fig. 3 A and B). Similarly, a single tamoxifen injection in Bmi1-CreER; Rosa26-YFP mice was used to irreversibly mark the Bmi1+ lineage, followed 2 d later by 12 Gy irradiation and tissue harvest at 7 d after irradiation. As opposed to the quantitative eradication of Lgr5+ ISC-derived progeny, irradiation substantially induced expansion of the Bmi1+ lineage. Indeed, by 7 d after irradiation in regenerating small intestine, confluent Bmi1+ ISC-derived YFP+ lineage stripes were seen along multiple adjacent crypts and villi, which were much more extensive than the comparatively atretic Bmi1+ lineage tracing present during homeostasis (Fig. 3 C and D and Fig. S2).

Strikingly, the Bmi1+ lineage showed postirradiation extension into multiple adjacent crypts and villi emanating from a single crypt as revealed by three-dimensional (3D) confocal reconstruction (Fig. 3 E–G and Movie S1). We also treated Bmi1-CreER; Rosa26-Confetti mice with tamoxifen 2 d before 12 Gy irradiation to stochastically label individual Bmi1+ ISCs with one of four possible fluorescent colors (4) and trace their fate in response to injury. Using this multicolor reporter to visualize the dramatic expansion of the Bmi1+ lineage, the progeny arising from the marked clones were noted to be exclusively labeled with a single color at 7 d after irradiation, attesting to their monoclonal origin despite their extension into contiguous crypts and villi (Fig. 3 H–K and Movie S2). Thus, compared with the radiosensitive, actively cycling Lgr5-eGFP+ ISCs, the quiescent Bmi1+ ISCs exhibit radioresistance and are rapidly mobilized to proliferate upon injury with significant contribution to epithelial regeneration, and pronounced induction of Bmi1+ lineage tracing. Taken together, these data suggest that Bmi1+ ISCs are quiescent...
Bmi1-YFP+ cells generated spheroids with similar morphology to niche (19, 20). To determine whether Bmi1+ ISCs can also form epithelial cells, representing Bmi1+ ISCs, from 1 or 2 d tamoxifen-suggest that Bmi1+ ISCs play a larger role during epithelial repair Cells in Vitro. Single Lgr5-eGFP+ ISCs can generate in vitro spheroids, we FACS-isolated single YFP+ small intestine injury. (A) Tamoxifen-mediated lineage trace of Lgr5-eGFP+ progeny in Lgr5-eGFP-IRES-CreERT2; Rosa-YFP mouse duodenum demonstrates proliferative lineage generation under homeostasis by 8 d (A). Lgr5-eGFP+ ISCs and their lineage are ablated at 7 d after 12 Gy whole-body irradiation (B). (C and D) Bmi1+ lineage in Bmi1-CreER; Rosa-YFP doubleum marked by 9-d tamoxifen treatment exhibits marked proliferative regenerative response with progeny observed in adjacent crypts and villi at 7 d after irradiation. (Scale bars: A–D, 100 μm.) Phalloidin is shown in red and DAPI in blue. (E–G) 3D confocal reconstruction of Bmi1+ lineage regenerative response in the jejunum at 7 d after 12 Gy irradiation highlights confluent patches of Bmi1+-derived cells in multiple adjacent crypts/villi. Zoomed view of regenerated jejunum immunostained with lysozyme, illustrating Paneth cells within a budding crypt (F). Phalloidin is colored in red and DAPI in blue. (H–K) Monoclonal repopulation of 7 d postirradiated jejunum from Bmi1-CreER; Rosa-Confetti compound heterozygotes, as suggested by monochromatic patches of regenerated crypts/villi illustrated in RFP (H), GFP (I), CFP (J), and YFP (K). Insets represent serial cross-sections through lineage traces indicating involvement of multiple contiguous crypts and villi (G and K).

at baseline but actively contribute to injury-associated repair upon quantitative loss of the Lgr5+ population or crypt injury and suggest that Bmi1+ ISCs play a larger role during epithelial repair than during basal homeostasis.

Isolated Bmi1+ ISCs Are Multipotent and Give Rise to Lgr5-Expressing Cells in Vitro. Single Lgr5-eGFP+ ISCs can generate in vitro spheroids in clonogenic culture without requiring a mesenchymal niche (19, 20). To determine whether Bmi1+ ISCs can also form in vitro spheroids, we FACS-isolated single YFP+ small intestine epithelial cells, representing Bmi1+ ISCs, from 1 or 2 d tamoxifen-treated Bmi1-CreER; Rosa26-YFP mice. These purified single Bmi1-YFP+ cells generated spheroids with similar morphology to Lgr5-eGFP-derived spheroids upon clonogenic culture in Matrigel with previously reported exogenous factors including Epidermal Growth Factor, Noggin, Jagged and Rspo1 (19) (Fig. 4 A–D and I and Fig. S3). Consistent with their in vivo stem cell function, the clonogenic spheroids grown from isolated Bmi1-YFP+ single cells exhibited multipotency (Fig. 4 E–H), continued proliferation (Fig. 4I), and maintenance of pan-YFP expression upon serial passage (>8 mo with weekly passages) (Fig. S3). Notably, numerous Lgr5+ cells were detected by Lgr5 mRNA fluorescence in situ hybridization (FISH) within the Bmi1+ clonally derived spheroids (Fig. 4K and Fig. S4), whose clonogenicity was confirmed by the genetic signature of pan-YFP expression seen by both intrinsic YFP fluorescence and immunodetection (Fig. 4 D and K), indicating that the Bmi1+ ISC lineage can generate Lgr5+ cells in vitro.

Discussion

Our findings reveal that under both homeostatic and injury-induced conditions, Bmi1 and Lgr5 mark functionally distinct ISC populations in vivo. Although Lgr5+ ISCs are extremely sensitive to Rspos1-mediated Wnt stimulation and Dkk1-mediated Wnt inhibition, Bmi1+ ISCs are relatively refractory to Wnt manipulation. Further, although Lgr5+ ISCs are actively cycling and quantitatively ablated by irradiation injury, the normally quiescent Bmi1+ ISCs are instead induced to proliferate upon irradiation and, in fact, give rise to progeny that clonally repopulate multiple contiguous crypt-villus axes during subsequent intestinal regeneration.

**Fig. 3.** Differential responses of Lgr5+ vs. Bmi1+ lineages to acute radiation injury. (A and B) Tamoxifen-mediated lineage trace of Lgr5-eGFP+ progeny in Lgr5-eGFP-IRES-CreERT2; Rosa-YFP mouse duodenum demonstrates proliferative lineage generation under homeostasis by 8 d (A). Lgr5-eGFP+ ISCs and their lineage are ablated at 7 d after 12 Gy whole-body irradiation (B). (C and D) Bmi1+ lineage in Bmi1-CreER; Rosa-YFP doubleum marked by 9-d tamoxifen treatment exhibits marked proliferative regenerative response with progeny observed in adjacent crypts and villi at 7 d after irradiation. (Scale bars: A–D, 100 μm.) Phalloidin is shown in red and DAPI in blue. (E–G) 3D confocal reconstruction of Bmi1+ lineage regenerative response in the jejunum at 7 d after 12 Gy irradiation highlights confluent patches of Bmi1+-derived cells in multiple adjacent crypts/villi. Zoomed view of regenerated jejunal immunostained with lysozyme, illustrating Paneth cells within a budding crypt (F). Phalloidin is colored in red and DAPI in blue. (H–K) Monoclonal repopulation of 7 d postirradiated jejunum from Bmi1-CreER; Rosa-Confetti compound heterozygotes, as suggested by monochromatic patches of regenerated crypts/villi illustrated in RFP (H), GFP (I), CFP (J), and YFP (K). Insets represent serial cross-sections through lineage traces indicating involvement of multiple contiguous crypts and villi (G and K).
Our results thus provide direct evidence that Bmi1+ ISCs represent a quiescent, injury-inducible reserve ISC population, consistent with a proposed model for coexistence of distinct ISC populations active during homeostasis vs. regeneration (10, 11, 21).

Tian and colleagues reported an elegant diphtheria toxin receptor (dTR) knock-in genetic strategy to selectively ablate Lgr5+ ISCs in vivo using diphtheria toxin, revealing that Lgr5+ ISCs are dispensable for intestinal homeostasis (9). Lgr5+ ISC ablation was accompanied by expansion of the Bmi1+ lineage, which is capable of giving rise to Lgr5-expressing cells in vivo (9). Their findings parallel and support our overall conclusions that the Bmi1+ lineage expands upon quantitative loss of the Lgr5+ population and of their lineage interrelationship. Notably, dTR-mediated genetic ablation of Lgr5+ ISCs differs from our radiation injury model because of the lack of crypt loss observed upon diphtheria toxin ablation. Moreover, the mediation of epithelial reconstitution by Bmi1+ ISCs after Lgr5+ ISC ablation by either dTR or radiation injury does not distinguish between models in which these two populations are either functionally redundant or alternatively possess distinct functions. Our data, which reveal profound differences between Bmi1+ and Lgr5+ ISCs in baseline quiescence, cell-cycle entry after injury, effects of Wnt gain- and loss-of-function, and radiosensitivity, strongly argue for the latter model.

Functional differences we describe therefore resolve the fundamental question of whether Bmi1+ and Lgr5+ ISCs are redundant or distinct populations and indicate that Bmi1+ ISC recruitment after injury marks the utilization of a functionally discrete ISC class. Finally, our findings of Bmi1+ ISC baseline quiescence and inducible proliferation after crypt injury provide functional evidence for Bmi1+ ISC as a postulated injury-mobilized population and further underscore the heterogeneity of ISC populations contributing to tissue regeneration.

It is certainly possible that Bmi1+ may only mark a subset of quiescent stem cells, and our results do not exclude overlapping expression with populations identified by other putative ISC molecular markers (8, 22–31), including those that may also function as quiescent and injury-mobilized ISCs. Additional proliferating cells not marked by Bmi1 are present in 2-d postirradiated crypts using our tamoxifen-labeling strategy, suggesting either variegated Bmi1 expression in our reporter system or the presence of further ISC populations. It is perhaps also mediate postinjury regional repair of the colon and distal small intestine. The relative scarcity of Bmi1+ ISCs may be insufficient to repair the entire intestinal epithelium after irradiation, and Bmi1+ ISC are not present in colon (2, 9). Other ISC markers have been proposed for identification of 4+ position quiescent cells including Dcmkl1 (28), mTert (8), and Hopx (32), and these cells themselves may exhibit heterogeneity because there are numerous cells occupying this crypt position within the annulus of the 3D crypt. Notably, mTert has been described to mark an ISC population at the 4+ position mobilized after radiation injury, and which overlaps in expression with both Lgr5 and Bmi1 (8, 33). Certainly, the potential overlap or interrelatedness of Bmi1+ and mTert+ ISC and other 4+ position markers such as Dcmkl1 and Hopx warrants further investigation. Further, the significance of overlapping Lgr5 coexpression within Bmi1+ ISCs (9) and the proportion of Bmi1+ mRNA-positive cells that are labeled by Bmi1-CreER remain to be determined.

Clonogenic cultures derived from isolated single Bmi1-YFP+ cells give rise to all differentiated intestinal lineages and Lgr5+ cells, supporting a lineage relationship where a quiescent ISC can give rise to an actively cycling ISC, and parallels in vivo observations of Lgr5+ cell generation from Bmi1+ ISCs (9). This work demonstrates clonogenic culture of the Bmi1+ ISC population. Intriguingly, upon removal from the native tissue microenvironment and FACS isolation, the normally quiescent Bmi1+ ISCs generate clonally derived intestinal spheroids with similar kinetics, morphology, and histology to those derived from single Lgr5+ ISCs (19). The self-renewal and proliferation of the Bmi1-derived spheroids, like those derived from Lgr5, are Rspo1-dependent, consistent with prior results with Bmi1+ lineage tracing in air-liquid interface organotypic cultures (17), whereas Bmi1+ ISCs are relatively insensitive to Rspo1-Fc in vivo. These results are potentially consistent with a model where Bmi1+ ISC are subject to considerable in vivo repression within the ISC niche, which does not appear to be recapitulated by current in vitro culture systems. Further, the clonogenic culture conditions used here, which were initially reported for Lgr5+ ISCs (19), may actually select for an actively cycling state. Despite their functional differences in vivo, we cannot completely exclude potential concomitant overlapping Lgr5 coexpression within Bmi1+ ISCs. It also remains to be determined whether the observed differences between the in vivo and in vitro properties are cell autonomous or due to differences in stem cell niche interactions.

Isolated Bmi1+ ISCs can give rise to Lgr5+ cells in vitro, and in vivo under homeostasis or dTR-mediated Lgr5+ cell ablation (9), although the frequency of this occurrence is unknown. This lineage could occur infrequently during homeostasis in vivo, given the relative paucity of Bmi1+ lineage contribution to basal regeneration. This lineage relationship could possibly also be bidirectional with Lgr5+ ISCs giving rise to Bmi1+ ISCs, paralleling the Lgr5/Hopx bidirectional relationship (32), with superimposed regulatory mechanisms to control the total number of ISCs, to regulate the balance of active and quiescent ISCs within the total stem cell pool, and to restrain homeostatic Bmi1+ ISC proliferation. Overall, our findings of multiple functional distinctions between Bmi1+ and Lgr5+ ISCs provide direct evidence to support a proposed model of separate but cooperative functional roles of multiple and distinct ISC populations (10, 11, 21) residing in adjacent niches that contribute to homeostatic vs. injury-induced regeneration, with Bmi1+ ISCs representing a quiescent, injury-inducible reserve ISC population. Further, the demonstration of Bmi1+ ISCs giving rise to Lgr5-expressing cells underscores the potentially complex interplay between these two populations.

**Materials and Methods**

Lgr5-eGFP-IRESCreERT2 mice were crossed with Rosa26-TdTomato or Rosa26-YFP to generate Lgr5-eGFP-IRESCreERT2; Rosa26-TdTomato or Lgr5-eGFP-IRESCreERT2; Rosa26-YFP compound heterozygotes, respectively. Likewise, Bmi1-CreER mice were crossed to Rosa26-YFP or Rosa26-Confetti to generate Bmi1-Cre;Rosa26-YFP or Bmi1-Cre;Rosa26-Confetti compound heterozygotes, respectively. Adult mice were injected with i.p. tamoxifen (Sigma) (9 mg per 40 g of body weight) to label Bmi1 ISCs and Bmi1+ and Lgr5+ lineages. For adenosine-mediated modulation of Wnt signaling, 5 × 10^6 p.f.u. of Ad Fc, Ad Rspo1-Fc, or Ad Dkk1 was injected (i.v.) per mouse. For irradiation injury studies, mice were given 12 Gy whole-body irradiation and tissue was harvested at multiple time points after irradiation injury. For proliferation studies, 1 mg of EdU (Invitrogen) was injected (i.p.) 4 h before killing and EdU incorporation was evaluated according to the manufacturer’s instructions with the Click-iT EdU imaging Kit (Invitrogen) on OCT (Tissue-Tek) frozen sections. FACS experiments were performed with fresh small intestine epithelial preparations isolated with 10 mM EDTA chelation (34) (Roche). For Bmi1-derived clonogenic cultures, 2- to 3-wk-old Bmi1-Cre;Rosa26-YFP mice were treated with tamoxifen as above. Tissue was dissociated into single cells for FACS isolation. Antibody staining was performed with anti-CD34, anti-CD31, and anti-EpCAM antibodies (eBioscience). CD34+ CD31− EpCAM+ YFP+ single cells were isolated by FACS and clonogenically cultured as described (19). FISH was performed on 6-μm paraffin-embedded Bmi1-derived clonogenic spheroids by using Lgr5 digoxigenin-labeled probes as described (17), with simultaneous immunodetection of YFP using anti-GFP antibody (Aves).

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Supporting Information

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SI Materials and Methods

Mice. Lgr5-eGFP-IRES-CreERT2 mice were crossed with Rosa26-TdTomato or Rosa26-YFP (JAX) mice to generate Lgr5-eGFP-IRES-CreERT2; Rosa26-TdTomato or Lgr5-eGFP-IRES-CreERT2; Rosa26-YFP compound heterozygous mice, respectively. Likewise, Bmi1-CreER mice were crossed to Rosa26-YFP or Rosa26-Confetti mice to generate Bmi1-CreER; Rosa26-YFP or Bmi1-CreER; Rosa26-Confetti compound heterozygous mice, respectively. Adult mice between 4–12 wk of age were administered IP tamoxifen (9 mg per 40 g of body weight) to label Bmi1 ISCs, and to label the Bmi1+ and Lgr5+ lineages, by using the various Rosa26 Cre reporter strains.

Proliferation Assay and Cell Quantitation. Bmi1+ ISCs were labeled in Bmi1-CreER; Rosa26-YFP double heterozygous mice with tamoxifen (i.p.) 24 h before sacrifice. Both Lgr5-eGFP-IRES-CreERT2 mice and tamoxifen-treated Bmi1-CreER; Rosa26-YFP mice were administered a single 1 mg injection (i.p.) of the thymidine analog EdU 4 h before killing. EdU incorporation was detected according to the manufacturer’s instructions with the Click-IT EdU Imaging Kit (Invitrogen) on OCT (Tissue Tek) frozen sections. All intestinal tissue was prepared as OCT frozen tissue blocks. Briefly, mouse intestine was fixed in 4% paraformaldehyde for 2–4 h, equilibrated into 30% sucrose, then embedded in OCT. Cryosections were cut at 8 μm. Proliferation indices are expressed as percentage of GFP+ or YFP+ epithelial cells that incorporated EdU over total number of GFP+ or YFP+ epithelial cells within proximal small intestine crypts. At least 50–100 total ISCs per mouse were counted from multiple fields. Statistical analysis was performed by using n = 3 mice for each condition. The mean and SEs are represented. Two-tailed P values were calculated by using unpaired Student’s t test. Lineage generation efficiency was quantified by calculating the percentage of GFP+ or YFP+ crypts or villi with three or more cells arising from Lgr5+ or Bmi1+ ISCs after 7-d tamoxifen treatment in Lgr5-eGFP-IRES-CreERT2; Rosa26-TdTomato or Bmi1-CreER; Rosa26-YFP mice, respectively. At least 100 total crypts and villi were counted from multiple fields. Statistical analysis was performed by using n = 3 mice for each condition. The mean and SE are represented. Two-tailed P values were calculated by using unpaired Student’s t test.

Wnt Modulation. Modulation of canonical Wnt signaling was achieved by 5 × 106 p.f.u. injection (i.v.) of Ad β-catenin or Ad β-catenin ΔN. Systemic infection was confirmed by histologic evaluation of the small intestine and immunolabel of the mouse sera for the presence of HA-epitope tagged soluble Rspo1-Fc and Dkk1 proteins. Mice were killed 5 d after infection. The small intestine was resected en bloc for histologic analysis as above.

Radiation Injury. Mice were administered 12 Gy of whole-body irradiation, and the tissue was harvested at multiple time points after irradiation and tamoxifen administration to label ISCs/their progeny. n = 3 mice or more were used for each condition. Tissue was fixed with 4% PFA as above and processed in OCT for frozen sections, paraffin, or prepared as whole mount.

Flow Cytometry. FACS experiments were performed by using fresh small intestine epithelial preparations. A standardized 3-cm segment of proximal jejunum was used for quantitative FACS analysis of ISC populations. Intestinal epithelial cells were extracted from en bloc resected small intestine with 10 mM EDTA and manual shaking, followed by enzymatic dissociation with collagenase/dispase (Roche) to generate a single-cell suspension (1). Singlet discrimination was sequentially performed by using plots for FSC (FSC-A vs. FSC-H) and SSC (SSC-W vs. SSC-H). Dead cells were excluded by scatter characteristics and propidium iodide. Epithelial cells were identified by CD45+ and EpCAM+ immunostaining. ISCs were identified by their endogenous GFP or YFP expression. All FACS experiments were performed on an Aria II sorter (BD Biosciences) at the Stanford University Shared FACS Facility, and FACS data were analyzed by using FlowJo software (TreeStar).

Clonogenic Culture. For Bmi1-derived clonogenic cultures, Bmi1-CreER; Rosa26-YFP mice were treated with tamoxifen as described above. Tissue was dissociated for FACS isolation as above. Singlet discrimination was sequentially performed by using plots for FSC (FSC-A vs. FSC-H) and SSC (SSC-W vs. SSC-H). Dead cells were excluded by scatter characteristics. Antibody staining was performed with anti-CD45, anti-CD31, and anti-EpCAM (eBiosciences). CD31+ CD45+ EpCAM+ YFP+ cells were isolated by FACS. These isolated cells were cultured and passaged once per week as described (2, 3). Lgr5-eGFP ISCs were also isolated from Lgr5-eGFP-IRES-CreERT2 mice by using the FACS gating scheme and culture methods reported by Sato et al. (2, 3).

Immunofluorescence. Paraffin-embedded sections were stained by using the following primary antibodies: anti-Muc2 (Santa Cruz), lysozyme (Dako), chromogranin A (Dako), E-cadherin (BD Biosciences), and sucrase-isomaltase (generated in house at Stanford University). All primary antibodies were used at 1:500. Cy3 and Cy5 conjugated secondary antibodies (Santa Cruz) were used at 1:2,000. Alexa Fluor 594-conjugated Phalloidin (Invitrogen) was used at 1:500. Images were captured on a Zeiss Axios Imager Z1 with ApoTome attachment or Leica CTR 6500 confocal microscope.

Lgr5 mRNA In Situ Hybridization. In situ hybridization was performed on 4% paraformaldehyde-fixed Bmi1-derived clonogenic intestinal spheroids by using 6-μm paraffin-embedded sections. For FISH, Lgr5 digoxigenin-labeled probes were synthesized as described (4). Sense strand probes were generated and served as negative controls. Simultaneous anti-YFP immunodetection was performed by using anti-GFP primary antibody (Aves) at 1:500, a FITC-conjugated secondary antibody (Aves) at 1:2,000 followed by further amplification using the TSA-Biotin system (Perkin-Elmer).

Ofm4 mRNA In Situ Hybridization by RNAscope. In situ hybridization for Ofm4 RNA was performed by using the RNAscope kit (Advanced Cell Diagnostics) according to the manufacturer’s instructions. Briefly, 5-μm formalin-fixed, paraffin-embedded tissue sections or 8-μm OCT frozen sections were pretreated with heat and protease before hybridization with a target probe to Ofm4 mRNA. An HRP-based signal amplification system was then hybridized to the target probes followed by colorimetric development with DAB. Positive staining was identified as brown, punctate dots present in the nucleus and/or cytoplasm. Negative control probes for the bacterial gene DapB were also included for each slide.

3D Confocal Reconstruction. Small intestine tissue samples were processed for immunofluorescence microscopy as described (5).
Briefly, samples were fixed with 2% paraformaldehyde for 1 h and permeabilized in PBS with 1% Triton X-100, 1% saponin, and 3% BSA. Bmi1-CreER; Rosa26-YFP samples were stained with DAPI and Phalloidin-Alexa Fluor 594 (Molecular Probes) and anti-lysozyme (Dako) for visualization of the nuclei, actin cytoskeleton, and Paneth cells, respectively. Bmi1-CreER; Rosa26-Confetti samples were not counterstained. For whole-mount visualization of intestine, samples were mounted as intact tissue blocks in Vectashield mounting medium (Vector Laboratories) and imaged with a Zeiss LSM 700 or Leica CTR 6500 confocal microscope. Z stacks were reconstructed into 3D by using Volocity (Improvision).

**Electron Microscopy.** Small intestine tissue samples were fixed with 2.5% glutaraldehyde and postfixed in 1% osmium tetroxide in 100 mM phosphate buffer. Tissue was dehydrated, embedded in epoxy resin, and visualized with a JEOL transmission electron microscope at 120 kV (model JEM-1210).


**Fig. S1.** Quantitative effects of canonical Wnt pathway modulation on Lgr5+ vs. Bmi1+ ISCs. (A–C) FACS analysis of Lgr5-eGFP+ ISCs in response to 5-d adenovirus treatment with Ad Fc, Ad Rspo1-Fc, or Ad Dkk1. Ad Rspo1-Fc expands whereas Ad Dkk1 ablates the Lgr5-eGFP+ ISC population by FACS. (D–F) In contrast, Bmi1+ ISCs labeled with 1.5-d tamoxifen treatment in Bmi1-CreER; Rosa26-YFP mice at 5 d after adenovirus injection are relatively insensitive to Wnt modulation with Ad Rspo1-Fc and Ad Dkk1 vs. Ad Fc. The proportion of Bmi1-YFP+ ISCs by FACS does not change relative to total number of CD45− and EpCAM+ intestinal epithelial cells with Wnt gain- and loss-of-function. (G–I) Effects of Ad Rspo1-Fc treatment on Bmi1+ lineage in vivo. Bmi1-CreER; Rosa26-YFP mice were treated with tamoxifen for 1.5 d then injected with adenovirus. Tissue was harvested 5 d after infection. No increase in Bmi1-derived lineage striping frequency was observed relative to Ad Fc, consistent with slow cycling of Bmi1+ ISCs that is not enhanced by Rspo1-mediated Wnt stimulation. Bmi1 lineage is colored in green and DAPI in blue. (Scale bars: 100 μm.)
Fig. S2. Bmi1+ lineage proliferates in response to irradiation injury. Bmi1-CreER; Rosa26-YFP mice were treated with tamoxifen for 2 d then given 12 Gy whole-body irradiation. By 7 d after irradiation injury (9 d total of tamoxifen exposure), there is marked Bmi1-derived proliferation in response to irradiation throughout the proximal small intestine that involves multiple contiguous crypts and villi. (Scale bars: 50 μm.)

Fig. S3. Serial passaging of Bmi1-YFP+ clonogenic spheroids. Representative spheroids derived from FACS-isolated Bmi1-YFP+ single cells, marked by tamoxifen administration for 1 or 2 d in Bmi1-CreER; Rosa26-YFP mice, after 8 mo of clonogenic culture and serial passaging. The spheroids were serially passaged weekly for 8 mo and maintained their morphology and pan-YFP expression. Lgr5+ ISCs with the highest GFP expression (denoted “Lgr5-eGFP<sup>Hi</sup>”) were isolated by FACS from Lgr5-eGFP-IRES-CreERT2 mouse small intestine and clonogenically cultured per previous reports (2) for direct comparison. (Scale bars: 100 μm.)
Fig. S4. Lgr5-expressing cells arise within Bmi1-YFP⁺ clonogenic spheroids. Multiple Lgr5-expressing cells were detected by Lgr5 mRNA FISH within FACS-isolated and clonally derived Bmi1-YFP⁺ spheroid, as revealed by simultaneous YFP immunodetection. The sense Lgr5 mRNA probe was used as a negative control. (Scale bars: 50 μm.)

Movie S1. 3D confocal reconstruction of Bmi1⁺ lineage expansion after irradiation. Bmi1-CreER; Rosa26-YFP mice were induced with 2-d tamoxifen exposure to irreversibly label Bmi1⁺ ISCs with YFP then subjected to 12 Gy whole-body irradiation. By 7 d after irradiation, multiple contiguous crypts and villi of the jejunum were repopulated by the Bmi1⁺ lineage (colored in green). Phalloidin is shown in red and DAPI in blue.
Movie S2. 3D confocal reconstruction of monoclonal expansion of Bmi1+ lineage after irradiation. Bmi1-CreER; Rosa26-Confetti mice were induced with 2-d tamoxifen exposure to stochastically label Bmi1+ ISCs with one of four possible fluorescent colors before 12 Gy irradiation. By 7 d after irradiation, progeny arising from the marked clones were exclusively labeled with a single color suggesting a monoclonal origin. Here the contiguous patch of crypts and villi of the repopulated jejunum arose from a clone stochastically marked with YFP (colored in yellow).